

#2

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,983

DATE: 12/19/2001

TIME: 16:47:19

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\12192001\J005983.raw

4 <110> APPLICANT: Allen, Keith D.  
 6 <120> TITLE OF INVENTION: TRANSGENIC MICE CONTAINING PERK PROTEIN  
 7 KINASE GENE DISRUPTIONS  
 10 <130> FILE REFERENCE: R-517  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/005,983  
 13 <141> CURRENT FILING DATE: 2001-11-07  
 15 <150> PRIOR APPLICATION NUMBER: US 60/246,676  
 16 <151> PRIOR FILING DATE: 2000-11-07  
 18 <150> PRIOR APPLICATION NUMBER: US 60/311,018  
 19 <151> PRIOR FILING DATE: 2001-08-08  
 21 <150> PRIOR APPLICATION NUMBER: US 60/324,765  
 22 <151> PRIOR FILING DATE: 2001-09-24  
 24 <150> PRIOR APPLICATION NUMBER: US 60/326,148  
 25 <151> PRIOR FILING DATE: 2001-09-28  
 27 <160> NUMBER OF SEQ ID NOS: 4  
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 4510  
 33 <212> TYPE: DNA  
 34 <213> ORGANISM: Mus musculus  
 36 <400> SEQUENCE: 1

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39 aggtcccgag cggcgatacg ggcgggcgcc gacggcaggg tctccatgcc cgcgcgtggg 180
40 gcgggcccgt gatggagcgc gccaccgcgc ccgggcccgc cgcgctgctg ctgcttctgt 240
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42 ctcccgcgtc ggagacagtg tttggcttag gggcagcggc cgcggcgact tcggccgcgc 360
43 ggggtgcctgc ggtggcaacg gccgaagtga ccgtggagga cgcggaggca ttgccggctg 420
44 ccgctggcga accggagtca cgcgcgacgg agcccgatga cgacgtggaa ctgcggcctc 480
45 gcggcaggtc cttggtaatc atcagcactt tagatggacg aatcgctgca ctggatgccg 540
46 agaattgatg gaaaaagcag tgggatttgg acgtggggtc tggttccttg gtttcatcta 600
47 gcctcagcaa gccagagggt tttgggaaca agatgatcat cccctccctg gatggagacc 660
48 tcttccagtg ggaccgggac cgagagagca tggaggccgt ccccttcacg gtggagtccc 720
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61 atgcaattat tcctctgccg acgatcaaat ggaagccctt aatccattct ccttctagga 1500
62 ctctgtcttt ggttgggtct gatgaatttg acaaatgtct aagtaatgat aagtattccc 1560

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63 acgaagaata cagtaatggt gcactttcaa tcttccagta tccatacgat aacggttact 1620
64 atctgccata ctacaagaga gaaaggaata agcggagcac gcagatcaca gtcaggttcc 1680
65 tggacagccc ccactacagc aagaacatcc gcaagaagga ccctatcctc ctgctgcact 1740
66 ggtggaagga gatattcggg acgatcctgc tttgcatcgt agccacgacc ttcctcgtgc 1800
67 gcaggctttt ccactcctcag cccacacaggc agcgggaagga gtctgaaact cagtgccaga 1860
68 ctgaaagtaa atacgactcc gtgagtgcg atgtcagtga caacagctgg aatgacatga 1920
69 agtactcagg atacgtatcc cgatatctaa cagattttga gccaatcag tgcattgggtc 1980
70 gtggtggctt tggcgtttgtc tttgaagcta aaaacaaagt agatgactgc aattacgcta 2040
71 tcaagaggat ccggtcctccc aacagggaagt tggcacggga gaaggtaatg cgggaagtta 2100
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73 cccacaccaga gaagtggcaa gaagagatgg atgagatctg gctcaaagac gaaagcacag 2220
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110 ctgaaatcaa tccatttggt ttggtggtgt acagaacgca cgtgaagtgtg ataactatta 4440
111 tgacttcttt caagtctaaa tgatttaata aaaaaatttt aaattaaaaa aaaaaaaaaa 4500

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4510

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112 aaaaaaaaaa
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 1114
116 <212> TYPE: PRT
117 <213> ORGANISM: Mus musculus
119 <400> SEQUENCE: 2
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121 1 5 10 15
122 Phe Leu Leu Leu Gly Cys Ala Ala Gly Ile Ser Ala Val Ala Pro Ala
123 20 25 30
124 Arg Ser Leu Leu Ala Pro Ala Ser Glu Thr Val Phe Gly Leu Gly Ala
125 35 40 45
126 Ala Ala Ala Pro Thr Ser Ala Ala Arg Val Pro Ala Val Ala Thr Ala
127 50 55 60
128 Glu Val Thr Val Glu Asp Ala Glu Ala Leu Pro Ala Ala Ala Gly Glu
129 65 70 75 80
130 Pro Glu Ser Arg Ala Thr Glu Pro Asp Asp Asp Val Glu Leu Arg Pro
131 85 90 95
132 Arg Gly Arg Ser Leu Val Ile Ile Ser Thr Leu Asp Gly Arg Ile Ala
133 100 105 110
134 Ala Leu Asp Ala Glu Asn Asp Gly Lys Lys Gln Trp Asp Leu Asp Val
135 115 120 125
136 Gly Ser Gly Ser Leu Val Ser Ser Ser Leu Ser Lys Pro Glu Val Phe
137 130 135 140
138 Gly Asn Lys Met Ile Ile Pro Ser Leu Asp Gly Asp Leu Phe Gln Trp
139 145 150 155 160
140 Asp Arg Asp Arg Glu Ser Met Glu Ala Val Pro Phe Thr Val Glu Ser
141 165 170 175
142 Leu Leu Glu Ser Ser Tyr Lys Phe Gly Asp Asp Val Val Leu Val Gly
143 180 185 190
144 Gly Lys Ser Leu Ile Thr Tyr Gly Leu Ser Ala Tyr Ser Gly Lys Leu
145 195 200 205
146 Arg Tyr Ile Cys Ser Ala Leu Gly Cys Arg Arg Trp Asp Ser Asp Glu
147 210 215 220
148 Met Glu Glu Glu Glu Asp Ile Leu Leu Leu Gln Arg Thr Gln Lys Thr
149 225 230 235 240
150 Val Arg Ala Val Gly Pro Arg Ser Gly Ser Glu Lys Trp Asn Phe Ser
151 245 250 255
152 Val Gly His Phe Glu Leu Arg Tyr Ile Pro Asp Met Glu Thr Arg Ala
153 260 265 270
154 Gly Phe Ile Glu Ser Thr Phe Lys Pro Gly Gly Asn Lys Glu Asp Ser
155 275 280 285
156 Lys Ile Ile Ser Asp Val Glu Glu Gln Glu Ala Thr Met Leu Asp Thr
157 290 295 300
158 Val Ile Lys Val Ser Val Ala Asp Trp Lys Val Met Ala Phe Ser Arg
159 305 310 315 320
160 Lys Gly Gly Arg Leu Glu Trp Glu Tyr Gln Phe Cys Thr Pro Ile Ala
161 325 330 335
162 Ser Ala Trp Leu Val Arg Asp Gly Lys Val Ile Pro Ile Ser Leu Phe

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163          340          345          350
164 Asp Asp Thr Ser Tyr Thr Ala Ser Glu Glu Ala Leu Gly Asp Glu Glu
165          355          360          365
166 Asp Ile Val Glu Ala Ala Arg Gly Ala Thr Glu Asn Ser Val Tyr Leu
167          370          375          380
168 Gly Met Tyr Arg Gly Gln Leu Tyr Leu Gln Ser Ser Val Arg Val Ser
169 385          390          395          400
170 Glu Lys Phe Pro Thr Ser Pro Lys Ala Leu Glu Ser Val Asn Gly Glu
171          405          410          415
172 Asn Ala Ile Ile Pro Leu Pro Thr Ile Lys Trp Lys Pro Leu Ile His
173          420          425          430
174 Ser Pro Ser Arg Thr Pro Val Leu Val Gly Ser Asp Glu Phe Asp Lys
175          435          440          445
176 Cys Leu Ser Asn Asp Lys Tyr Ser His Glu Glu Tyr Ser Asn Gly Ala
177          450          455          460
178 Leu Ser Ile Leu Gln Tyr Pro Tyr Asp Asn Gly Tyr Tyr Leu Pro Tyr
179 465          470          475          480
180 Tyr Lys Arg Glu Arg Asn Lys Arg Ser Thr Gln Ile Thr Val Arg Phe
181          485          490          495
182 Leu Asp Ser Pro His Tyr Ser Lys Asn Ile Arg Lys Lys Asp Pro Ile
183          500          505          510
184 Leu Leu Leu His Trp Trp Lys Glu Ile Phe Gly Thr Ile Leu Leu Cys
185          515          520          525
186 Ile Val Ala Thr Thr Phe Ile Val Arg Arg Leu Phe His Pro Gln Pro
187          530          535          540
188 His Arg Gln Arg Lys Glu Ser Glu Thr Gln Cys Gln Thr Glu Ser Lys
189 545          550          555          560
190 Tyr Asp Ser Val Ser Ala Asp Val Ser Asp Asn Ser Trp Asn Asp Met
191          565          570          575
192 Lys Tyr Ser Gly Tyr Val Ser Arg Tyr Leu Thr Asp Phe Glu Pro Ile
193          580          585          590
194 Gln Cys Met Gly Arg Gly Gly Phe Gly Val Val Phe Glu Ala Lys Asn
195          595          600          605
196 Lys Val Asp Asp Cys Asn Tyr Ala Ile Lys Arg Ile Arg Leu Pro Asn
197          610          615          620
198 Arg Glu Leu Ala Arg Glu Lys Val Met Arg Glu Val Lys Ala Leu Ala
199 625          630          635          640
200 Lys Leu Glu His Pro Gly Ile Val Arg Tyr Phe Asn Ala Trp Leu Glu
201          645          650          655
202 Thr Pro Pro Glu Lys Trp Gln Glu Glu Met Asp Glu Ile Trp Leu Lys
203          660          665          670
204 Asp Glu Ser Thr Asp Trp Pro Leu Ser Ser Pro Ser Pro Met Asp Ala
205          675          680          685
206 Pro Ser Val Lys Ile Arg Arg Met Asp Pro Phe Ser Thr Lys Glu Gln
207          690          695          700
208 Ile Glu Val Ile Ala Pro Ser Pro Glu Arg Ser Arg Ser Phe Ser Val
209 705          710          715          720
210 Gly Ile Ser Cys Gly Gln Thr Ser Ser Ser Glu Ser Gln Phe Ser Pro
211          725          730          735

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212 Leu Glu Phe Ser Gly Thr Asp Cys Gly Asp Asn Ser Asp Ser Ala Asp
213              740              745              750
214 Ala Ala Tyr Asn Leu Gln Asp Ser Cys Leu Thr Asp Cys Glu Asp Val
215              755              760              765
216 Glu Asp Gly Thr Val Asp Gly Asn Asp Glu Gly His Ser Phe Glu Leu
217              770              775              780
218 Cys Pro Ser Glu Ala Ser Pro Tyr Thr Arg Ser Arg Glu Gly Thr Ser
219 785              790              795              800
220 Ser Ser Ile Val Phe Glu Asp Ser Gly Cys Gly Asn Ala Ser Ser Lys
221              805              810              815
222 Glu Glu Pro Arg Gly Asn Arg Leu His Asp Gly Asn His Tyr Val Asn
223              820              825              830
224 Lys Leu Thr Asp Leu Lys Cys Ser Ser Ser Arg Ser Ser Glu Ala
225              835              840              845
226 Thr Thr Leu Ser Thr Ser Pro Thr Arg Pro Thr Thr Leu Ser Leu Asp
227              850              855              860
228 Phe Thr Lys Asn Thr Val Gly Gln Leu Gln Pro Ser Ser Pro Lys Val
229 865              870              875              880
230 Tyr Leu Tyr Ile Gln Met Gln Leu Cys Arg Lys Glu Asn Leu Lys Asp
231              885              890              895
232 Trp Met Asn Arg Arg Cys Ser Leu Glu Asp Arg Glu His Gly Val Cys
233              900              905              910
234 Leu His Ile Phe Leu Gln Ile Ala Glu Ala Val Glu Phe Leu His Ser
235              915              920              925
236 Lys Gly Leu Met His Arg Asp Leu Lys Pro Ser Asn Ile Phe Phe Thr
237              930              935              940
238 Met Asp Asp Val Val Lys Val Gly Asp Phe Gly Leu Val Thr Ala Met
239 945              950              955              960
240 Asp Gln Asp Glu Glu Gln Thr Val Leu Thr Pro Met Pro Ala Tyr
241              965              970              975
242 Ala Thr His Thr Gly Gln Val Gly Thr Lys Leu Tyr Met Ser Pro Glu
243              980              985              990
244 Gln Ile His Gly Asn Asn Tyr Ser His Lys Val Asp Ile Phe Ser Leu
245              995              1000              1005
246 Gly Leu Ile Leu Phe Glu Leu Leu Tyr Pro Phe Ser Thr Gln Met Glu
247              1010              1015              1020
248 Arg Val Arg Ile Leu Thr Asp Val Arg Asn Leu Lys Phe Pro Leu Leu
249 1025              1030              1035              1040
250 Phe Thr Gln Lys Tyr Pro Gln Glu His Met Met Val Gln Asp Met Leu
251              1045              1050              1055
252 Ser Pro Ser Pro Thr Glu Arg Pro Glu Ala Thr Asp Ile Ile Glu Asn
253              1060              1065              1070
254 Ala Ile Phe Glu Asn Leu Glu Phe Pro Gly Lys Thr Val Leu Arg Gln
255              1075              1080              1085
256 Arg Ser Arg Ser Met Ser Ser Ser Gly Thr Lys His Ser Arg Gln Pro
257              1090              1095              1100
258 Ser Cys Ser Tyr Ser Pro Leu Pro Gly Asn
259 1105              1110
262 <210> SEQ ID NO: 3

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number